

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 09/696,709  
Source: IFW16  
Date Processed by STIC: 11-10-2004

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IFW16

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/696,709

DATE: 11/10/2004

TIME: 10:22:27

Input Set : N:\Crf3\RULE60\09696709.raw.txt  
 Output Set: N:\CRF4\11102004\I696709.raw

## SEQUENCE LISTING

## 3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Lambert, Lewis H., Jr.  
 7 (ii) TITLE OF INVENTION: Improved Therapeutic Compositions Comprising  
 8 Bactericidal/Permeability-Increasing (BPI) Protein

Products

10 (iii) NUMBER OF SEQUENCES: 2  
 12 (iv) CORRESPONDENCE ADDRESS:  
 13 (A) ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
 14 (B) STREET: 6300 Sears Tower, 233 South Wacker Drive  
 15 (C) CITY: Chicago  
 16 (D) STATE: Illinois  
 17 (E) COUNTRY: United States of America  
 18 (F) ZIP: 60606-6402  
 20 (v) COMPUTER READABLE FORM:  
 21 (A) MEDIUM TYPE: Floppy disk  
 22 (B) COMPUTER: IBM PC compatible  
 23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
 24 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

26 (vi) CURRENT APPLICATION DATA:  
 27 (A) APPLICATION NUMBER: US/09/696,709

C--> 27 (B) FILING DATE: 24-Oct-2000  
 C--> 28 (C) CLASSIFICATION: 514

W--> 36 (vii) PRIOR APPLICATION DATA:

31 (A) APPLICATION NUMBER: US/08/586,133  
 W--> 32 (B) FILING DATE: 12-JAN-1996  
 33 (C) APPLICATION NUMBER: US 08/372,104

W--> 34 (B) FILING DATE: 13-JAN-1995

35 (viii) ATTORNEY/AGENT INFORMATION:  
 38 (A) NAME: Sharp, Jeffrey S.  
 39 (B) REGISTRATION NUMBER: 31,879  
 40 (C) REFERENCE/DOCKET NUMBER: 27129/33071

43 (ix) TELECOMMUNICATION INFORMATION:  
 44 (A) TELEPHONE: 312/474-6300  
 45 (B) TELEFAX: 312/474-0448  
 46 (C) TELEX: 25-3856

## 49 (2) INFORMATION FOR SEQ ID NO: 1:

51 (i) SEQUENCE CHARACTERISTICS:  
 52 (A) LENGTH: 1813 base pairs  
 53 (B) TYPE: nucleic acid  
 54 (C) STRANDEDNESS: single  
 55 (D) TOPOLOGY: linear  
 57 (ii) MOLECULE TYPE: cDNA  
 60 (ix) FEATURE:

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61 (A) NAME/KEY: CDS  
62 (B) LOCATION: 31..1491  
64 (ix) FEATURE:  
65 (A) NAME/KEY: mat\_peptide  
66 (B) LOCATION: 124..1491  
68 (ix) FEATURE:  
69 (A) NAME/KEY: misc\_feature  
71 (D) OTHER INFORMATION: "rBPI"  
74 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
76 CAGGCCTTGA GGTTTTGGCA GCTCTGGAGG ATG AGA GAG AAC ATG GCC AGG GGC 54  
77 Met Arg Glu Asn Met Ala Arg Gly  
78 -31 -30 -25  
80 CCT TGC AAC GCG CCG AGA TGG GTG TCC CTG ATG GTG CTC GTC GCC ATA 102  
81 Pro Cys Asn Ala Pro Arg Trp Val Ser Leu Met Val Leu Val Ala Ile  
82 -20 -15 -10  
84 GGC ACC GCC GTG ACA GCG GCC GTC AAC CCT GGC GTC GTG GTC AGG ATC 150  
85 Gly Thr Ala Val Thr Ala Ala Val Asn Pro Gly Val Val Arg Ile  
86 -5 1 5  
88 TCC CAG AAG GGC CTG GAC TAC GCC AGC CAG CAG GGG ACG GCC GCT CTG 198  
89 Ser Gln Lys Gly Leu Asp Tyr Ala Ser Gln Gln Gly Thr Ala Ala Leu  
90 10 15 20 25  
92 CAG AAG GAG CTG AAG AGG ATC AAG ATT CCT GAC TAC TCA GAC AGC TTT 246  
93 Gln Lys Glu Leu Lys Arg Ile Lys Ile Pro Asp Tyr Ser Asp Ser Phe  
94 30 35 40  
96 AAG ATC AAG CAT CTT GGG AAG GGG CAT TAT AGC TTC TAC AGC ATG GAC 294  
97 Lys Ile Lys His Leu Gly Lys Gly His Tyr Ser Phe Tyr Ser Met Asp  
98 45 50 55  
100 ATC CGT GAA TTC CAG CTT CCC AGT TCC CAG ATA AGC ATG GTG CCC AAT 342  
101 Ile Arg Glu Phe Gln Leu Pro Ser Ser Gln Ile Ser Met Val Pro Asn  
102 60 65 70  
104 GTG GGC CTT AAG TTC TCC ATC AGC AAC GCC AAT ATC AAG ATC AGC GGG 390  
105 Val Gly Leu Lys Phe Ser Ile Ser Asn Ala Asn Ile Lys Ile Ser Gly  
106 75 80 85  
108 AAA TGG AAG GCA CAA AAG AGA TTC TTA AAA ATG AGC GGC AAT TTT GAC 438  
109 Lys Trp Lys Ala Gln Lys Arg Phe Leu Lys Met Ser Gly Asn Phe Asp  
110 90 95 100 105  
112 CTG AGC ATA GAA GGC ATG TCC ATT TCG GCT GAT CTG AAG CTG GGC AGT 486  
113 Leu Ser Ile Glu Gly Met Ser Ile Ser Ala Asp Leu Lys Leu Gly Ser  
114 110 115 120  
116 AAC CCC ACG TCA GGC AAG CCC ACC ATC ACC TGC TCC AGC TGC AGC AGC 534  
117 Asn Pro Thr Ser Gly Lys Pro Thr Ile Thr Cys Ser Ser Cys Ser Ser  
118 125 130 135  
120 CAC ATC AAC AGT GTC CAC GTG CAC ATC TCA AAG AGC AAA GTC GGG TGG 582  
121 His Ile Asn Ser Val His Val His Ile Ser Lys Ser Lys Val Gly Trp  
122 140 145 150  
124 CTG ATC CAA CTC TTC CAC AAA AAA ATT GAG TCT GCG CTT CGA AAC AAG 630  
125 Leu Ile Gln Leu Phe His Lys Lys Ile Glu Ser Ala Leu Arg Asn Lys  
126 155 160 165  
128 ATG AAC AGC CAG GTC TGC GAG AAA GTG ACC AAT TCT GTA TCC TCC AAG 678

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129	Met	Asn	Ser	Gln	Val	Cys	Glu	Lys	Val	Thr	Asn	Ser	Val	Ser	Ser	Lys	
130	170				175				180							185	
132	CTG	CAA	CCT	TAT	TTC	CAG	ACT	CTG	CCA	GTA	ATG	ACC	AAA	ATA	GAT	TCT	726
133	Leu	Gln	Pro	Tyr	Phe	Gln	Thr	Leu	Pro	Val	Met	Thr	Lys	Ile	Asp	Ser	
134						190				195						200	
136	GTG	GCT	GGA	ATC	AAC	TAT	GGT	CTG	GTG	GCA	CCT	CCA	GCA	ACC	ACG	GCT	774
137	Val	Ala	Gly	Ile	Asn	Tyr	Gly	Leu	Ala	Pro	Pro	Ala	Thr	Thr	Ala		
138						205			210							215	
140	GAG	ACC	CTG	GAT	GTA	CAG	ATG	AAG	GGG	GAG	TTT	TAC	AGT	GAG	AAC	CAC	822
141	Glu	Thr	Leu	Asp	Val	Gln	Met	Lys	Gly	Glu	Phe	Tyr	Ser	Glu	Asn	His	
142						220			225							230	
144	CAC	AAT	CCA	CCT	CCC	TTT	GCT	CCA	CCA	GTG	ATG	GAG	TTT	CCC	GCT	GCC	870
145	His	Asn	Pro	Pro	Pro	Phe	Ala	Pro	Pro	Val	Met	Glu	Phe	Pro	Ala	Ala	
146						235			240							245	
148	CAT	GAC	CGC	ATG	GTA	TAC	CTG	GGC	CTC	TCA	GAC	TAC	TTC	TTC	AAC	ACA	918
149	His	Asp	Arg	Met	Val	Tyr	Leu	Gly	Leu	Ser	Asp	Tyr	Phe	Phe	Asn	Thr	
150						250			255							265	
152	GCC	GGG	CTT	GTA	TAC	CAA	GAG	GCT	GGG	GTC	TTG	AAG	ATG	ACC	CTT	AGA	966
153	Ala	Gly	Leu	Val	Tyr	Gln	Glu	Ala	Gly	Val	Leu	Lys	Met	Thr	Leu	Arg	
154						270			275							280	
156	GAT	GAC	ATG	ATT	CCA	AAG	GAG	TCC	AAA	TTT	CGA	CTG	ACA	ACC	AAG	TTC	1014
157	Asp	Asp	Met	Ile	Pro	Lys	Glu	Ser	Lys	Phe	Arg	Leu	Thr	Thr	Lys	Phe	
158						285			290							295	
160	TTT	GGA	ACC	TTC	CTA	CCT	GAG	GTG	GCC	AAG	AAG	TTT	CCC	AAC	ATG	AAG	1062
161	Phe	Gly	Thr	Phe	Leu	Pro	Glu	Val	Ala	Lys	Lys	Phe	Pro	Asn	Met	Lys	
162						300			305							310	
164	ATA	CAG	ATC	CAT	GTC	TCA	GCC	TCC	ACC	CCG	CCA	CAC	CTG	TCT	GTG	CAG	1110
165	Ile	Gln	Ile	His	Val	Ser	Ala	Ser	Thr	Pro	Pro	His	Leu	Ser	Val	Gln	
166						315			320							325	
168	CCC	ACC	GGC	CTT	ACC	TTC	TAC	CCT	GCC	GTG	GAT	GTC	CAG	GCC	TTT	GCC	1158
169	Pro	Thr	Gly	Leu	Thr	Phe	Tyr	Pro	Ala	Val	Asp	Val	Gln	Ala	Phe	Ala	
170						330			335							345	
172	GTC	CTC	CCC	AAC	TCC	TCC	CTG	GCT	TCC	CTC	TTC	CTG	ATT	GGC	ATG	CAC	1206
173	Val	Leu	Pro	Asn	Ser	Ser	Leu	Ala	Ser	Leu	Phe	Leu	Ile	Gly	Met	His	
174						350			355							360	
176	ACA	ACT	GGT	TCC	ATG	GAG	GTC	AGC	GCC	GAG	TCC	AAC	AGG	CTT	GTT	GGA	1254
177	Thr	Thr	Gly	Ser	Met	Glu	Val	Ser	Ala	Glu	Ser	Asn	Arg	Leu	Val	Gly	
178						365			370							375	
180	GAG	CTC	AAG	CTG	GAT	AGG	CTG	CTC	GAA	CTG	AAG	CAC	TCA	AAT	ATT		1302
181	Glu	Leu	Lys	Leu	Asp	Arg	Leu	Leu	Leu	Glu	Leu	Lys	His	Ser	Asn	Ile	
182						380			385							390	
184	GGC	CCC	TTC	CCG	GTT	GAA	TTG	CTG	CAG	GAT	ATC	ATG	AAC	TAC	ATT	GTA	1350
185	Gly	Pro	Phe	Pro	Val	Glu	Leu	Leu	Gln	Asp	Ile	Met	Asn	Tyr	Ile	Val	
186						395			400							405	
188	CCC	ATT	CTT	GTG	CTG	CCC	AGG	GTT	AAC	GAG	AAA	CTA	CAG	AAA	GGC	TTC	1398
189	Pro	Ile	Leu	Val	Leu	Pro	Arg	Val	Asn	Glu	Lys	Leu	Gln	Lys	Gly	Phe	
190						410			415							420	
192	CCT	CTC	CCG	ACG	CCG	GCC	AGA	GTC	CAG	CTC	TAC	AAC	GTA	GTG	CTT	CAG	1446
193	Pro	Leu	Pro	Thr	Pro	Ala	Arg	Val	Gln	Leu	Tyr	Asn	Val	Val	Leu	Gln	

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194	430	435	440	
196	CCT CAC CAG AAC TTC CTG CTG TTC GGT GCA GAC GTT GTC TAT AAA			1491
197	Pro His Gln Asn Phe Leu Leu Phe Gly Ala Asp Val Val Tyr Lys			
198	445	450	455	
200	TGAAGGCACC AGGGGTGCCG GGGGCTGTCA GCCGCACCTG TTCCTGATGG GCTGTGGGC			1551
202	ACCGGCTGCC TTTCCCCAGG GAATCCTCTC CAGATCTTAA CCAAGAGCCC CTTGCAAAC			1611
204	TCTTCGACTC AGATTCAAGAA ATGATCTAAA CACGAGGAAA CATTATTCTAT TGGAAAAGTG			1671
206	CATGGTGTGT ATTTTAGGGA TTATGAGCTT CTTTCAAGGG CTAAGGCTGC AGAGATATTT			1731
208	CCTCCAGGAA TCGTGTTCATTGTAACCA AGAAATTCC ATTGTGCTT CATGAAAAAA			1791
210	AACTTCTGGT TTTTTTCATG TG			1813
213	(2) INFORMATION FOR SEQ ID NO: 2:			
215	(i) SEQUENCE CHARACTERISTICS:			
216	(A) LENGTH: 487 amino acids			
217	(B) TYPE: amino acid			
218	(D) TOPOLOGY: linear			
220	(ii) MOLECULE TYPE: protein			
222	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:			
224	Met Arg Glu Asn Met Ala Arg Gly Pro Cys Asn Ala Pro Arg Trp Val			
225	-31 -30	-25	-20	
227	Ser Leu Met Val Leu Val Ala Ile Gly Thr Ala Val Thr Ala Ala Val			
228	-15	-10	-5	1
230	Asn Pro Gly Val Val Val Arg Ile Ser Gln Lys Gly Leu Asp Tyr Ala			
231	5	10	15	
233	Ser Gln Gln Gly Thr Ala Ala Leu Gln Lys Glu Leu Lys Arg Ile Lys			
234	20	25	30	
236	Ile Pro Asp Tyr Ser Asp Ser Phe Lys Ile Lys His Leu Gly Lys Gly			
237	35	40	45	
239	His Tyr Ser Phe Tyr Ser Met Asp Ile Arg Glu Phe Gln Leu Pro Ser			
240	50	55	60	65
242	Ser Gln Ile Ser Met Val Pro Asn Val Gly Leu Lys Phe Ser Ile Ser			
243	70	75	80	
245	Asn Ala Asn Ile Lys Ile Ser Gly Lys Trp Lys Ala Gln Lys Arg Phe			
246	85	90	95	
248	Leu Lys Met Ser Gly Asn Phe Asp Leu Ser Ile Glu Gly Met Ser Ile			
249	100	105	110	
251	Ser Ala Asp Leu Lys Leu Gly Ser Asn Pro Thr Ser Gly Lys Pro Thr			
252	115	120	125	
254	Ile Thr Cys Ser Ser Cys Ser Ser His Ile Asn Ser Val His Val His			
255	130	135	140	145
257	Ile Ser Lys Ser Lys Val Gly Trp Leu Ile Gln Leu Phe His Lys Lys			
258	150	155	160	
260	Ile Glu Ser Ala Leu Arg Asn Lys Met Asn Ser Gln Val Cys Glu Lys			
261	165	170	175	
263	Val Thr Asn Ser Val Ser Ser Lys Leu Gln Pro Tyr Phe Gln Thr Leu			
264	180	185	190	
266	Pro Val Met Thr Lys Ile Asp Ser Val Ala Gly Ile Asn Tyr Gly Leu			
267	195	200	205	
269	Val Ala Pro Pro Ala Thr Thr Ala Glu Thr Leu Asp Val Gln Met Lys			
270	210	215	220	225

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272 Gly Glu Phe Tyr Ser Glu Asn His His Asn Pro Pro Pro Phe Ala Pro  
273 230 235 240  
275 Pro Val Met Glu Phe Pro Ala Ala His Asp Arg Met Val Tyr Leu Gly  
276 245 250 255  
278 Leu Ser Asp Tyr Phe Phe Asn Thr Ala Gly Leu Val Tyr Gln Glu Ala  
279 260 265 270  
281 Gly Val Leu Lys Met Thr Leu Arg Asp Asp Met Ile Pro Lys Glu Ser  
282 275 280 285  
284 Lys Phe Arg Leu Thr Thr Lys Phe Phe Gly Thr Phe Leu Pro Glu Val  
285 290 295 300 305  
287 Ala Lys Lys Phe Pro Asn Met Lys Ile Gln Ile His Val Ser Ala Ser  
288 310 315 320  
290 Thr Pro Pro His Leu Ser Val Gln Pro Thr Gly Leu Thr Phe Tyr Pro  
291 325 330 335  
293 Ala Val Asp Val Gln Ala Phe Ala Val Leu Pro Asn Ser Ser Leu Ala  
294 340 345 350  
296 Ser Leu Phe Leu Ile Gly Met His Thr Thr Gly Ser Met Glu Val Ser  
297 355 360 365  
299 Ala Glu Ser Asn Arg Leu Val Gly Glu Leu Lys Leu Asp Arg Leu Leu  
300 370 375 380 385  
302 Leu Glu Leu Lys His Ser Asn Ile Gly Pro Phe Pro Val Glu Leu Leu  
303 390 395 400  
305 Gln Asp Ile Met Asn Tyr Ile Val Pro Ile Leu Val Leu Pro Arg Val  
306 405 410 415  
308 Asn Glu Lys Leu Gln Lys Gly Phe Pro Leu Pro Thr Pro Ala Arg Val  
309 420 425 430  
311 Gln Leu Tyr Asn Val Val Leu Gln Pro His Gln Asn Phe Leu Leu Phe  
312 435 440 445  
314 Gly Ala Asp Val Val Tyr Lys  
315 450 455

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/696,709

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Input Set : N:\Crf3\RULE60\09696709.raw.txt

Output Set: N:\CRF4\11102004\I696709.raw

L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:34 M:238 W: Alpha Fields not Ordered, Reordered [(A) APPLICATION NUMBER:] of (1) (vii)  
L:36 M:238 W: Alpha Fields not Ordered, Reordered [(C) CLASSIFICATION:] of (1) (vi)